

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/725,037
Source: IFW0
Date Processed by STIC: 10/18/04

ENTERED



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/725,037

DATE: 10/18/2004

TIME: 10:28:10

Input Set : A:\78031566.app

Output Set: N:\CRF4\10182004\J725037.raw

3 <110> APPLICANT: ZOLLER, MARK
 4 LI, XIAODONG
 5 STASZEWSKI, LENA
 6 O'CONNELL, SHAWN
 7 ZOZULYA, SERGEY
 8 ADLER, JON
 9 XU, HONG
 10 ECHEVERRI, FERNANDO
 12 <120> TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
 13 THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
 14 IDENTIFICATION OF TASTE COMPOUNDS
 16 <130> FILE REFERENCE: 078003-0291566
 --> 18 <140> CURRENT APPLICATION NUMBER: US/10/725,037
 --> 19 <141> CURRENT FILING DATE: 2003-12-02
 21 <150> PRIOR APPLICATION NUMBER: 60/300,434
 22 <151> PRIOR FILING DATE: 2001-06-26
 24 <150> PRIOR APPLICATION NUMBER: 60/304,749
 25 <151> PRIOR FILING DATE: 2001-07-13
 27 <150> PRIOR APPLICATION NUMBER: 60/310,493
 28 <151> PRIOR FILING DATE: 2001-08-08
 30 <150> PRIOR APPLICATION NUMBER: 60/331,771
 31 <151> PRIOR FILING DATE: 2001-11-21
 33 <150> PRIOR APPLICATION NUMBER: 60/339,472
 34 <151> PRIOR FILING DATE: 2001-12-14
 36 <150> PRIOR APPLICATION NUMBER: 60/372,090
 37 <151> PRIOR FILING DATE: 2002-04-15
 39 <150> PRIOR APPLICATION NUMBER: 60/374,143
 40 <151> PRIOR FILING DATE: 2002-04-22
 42 <160> NUMBER OF SEQ ID NOS: 19
 44 <170> SOFTWARE: PatentIn Ver. 2.1
 46 <210> SEQ ID NO: 1
 47 <211> LENGTH: 5
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Description of Artificial Sequence: PDZIP sequence
 54 <400> SEQUENCE: 1
 55 Ser Val Ser Thr Trp
 56 1 5
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 14
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Artificial Sequence

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64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
66     sequence
68 <220> FEATURE:
69 <221> NAME/KEY: MOD_RES
70 <222> LOCATION: (1)
71 <223> OTHER INFORMATION: Thr or Arg
73 <220> FEATURE:
74 <221> NAME/KEY: MOD_RES
75 <222> LOCATION: (3)
76 <223> OTHER INFORMATION: Phe or Leu
78 <220> FEATURE:
79 <221> NAME/KEY: MOD_RES
80 <222> LOCATION: (4)
81 <223> OTHER INFORMATION: Arg, Gln or Pro
83 <220> FEATURE:
84 <221> NAME/KEY: MOD_RES
85 <222> LOCATION: (6)
86 <223> OTHER INFORMATION: Arg or Thr
88 <220> FEATURE:
89 <221> NAME/KEY: MOD_RES
90 <222> LOCATION: (7)
91 <223> OTHER INFORMATION: Ser, Pro or Val
93 <220> FEATURE:
94 <221> NAME/KEY: MOD_RES
95 <222> LOCATION: (8)
96 <223> OTHER INFORMATION: Val, Glu, Arg, Lys or Thr
98 <220> FEATURE:
99 <221> NAME/KEY: MOD_RES
100 <222> LOCATION: (11)
101 <223> OTHER INFORMATION: Ala or Glu
103 <220> FEATURE:
104 <221> NAME/KEY: MOD_RES
105 <222> LOCATION: (12)
106 <223> OTHER INFORMATION: Trp or Leu
108 <220> FEATURE:
109 <221> NAME/KEY: MOD_RES
110 <222> LOCATION: (13)
111 <223> OTHER INFORMATION: Arg, His or Gly
113 <400> SEQUENCE: 2
-> 114 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
115     1             5             10
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 15
120 <212> TYPE: PRT
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
125     sequence

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127 <220> FEATURE:
128 <221> NAME/KEY: MOD_RES
129 <222> LOCATION: (1)
130 <223> OTHER INFORMATION: Leu or Gln
132 <220> FEATURE:
133 <221> NAME/KEY: MOD_RES
134 <222> LOCATION: (3)
135 <223> OTHER INFORMATION: Glu, Gly or Thr
137 <220> FEATURE:
138 <221> NAME/KEY: MOD_RES
139 <222> LOCATION: (4)
140 <223> OTHER INFORMATION: Asn, Arg or Cys
142 <220> FEATURE:
143 <221> NAME/KEY: MOD_RES
144 <222> LOCATION: (7)
145 <223> OTHER INFORMATION: Arg or Glu
147 <220> FEATURE:
148 <221> NAME/KEY: MOD_RES
149 <222> LOCATION: (9)
150 <223> OTHER INFORMATION: Arg or Lys
152 <220> FEATURE:
153 <221> NAME/KEY: MOD_RES
154 <222> LOCATION: (10)
155 <223> OTHER INFORMATION: Cys, Gly or Phe
157 <220> FEATURE:
158 <221> NAME/KEY: MOD_RES
159 <222> LOCATION: (11)
160 <223> OTHER INFORMATION: Val, Leu or Ile
162 <220> FEATURE:
163 <221> NAME/KEY: MOD_RES
164 <222> LOCATION: (13)
165 <223> OTHER INFORMATION: Phe or Leu
167 <220> FEATURE:
168 <221> NAME/KEY: MOD_RES
169 <222> LOCATION: (14)
170 <223> OTHER INFORMATION: Ala or Ser
172 <220> FEATURE:
173 <221> NAME/KEY: MOD_RES
174 <222> LOCATION: (15)
175 <223> OTHER INFORMATION: Met or Leu
177 <400> SEQUENCE: 3
-> 178 Xaa Pro Xaa Xaa Tyr Asn Xaa Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa
179      1              5              10              15
182 <210> SEQ ID NO: 4
183 <211> LENGTH: 858
184 <212> TYPE: PRT
185 <213> ORGANISM: Rattus sp.
187 <400> SEQUENCE: 4
188 Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu

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```

189      1              5              10              15
191 Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
192              20              25              30
194 Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu
195              35              40              45
197 Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg
198              50              55              60
200 Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
201      65              70              75              80
203 Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
204              85              90              95
206 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro
207              100              105              110
209 Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
210              115              120              125
212 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
213      130              135              140
215 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
216 145              150              155              160
218 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
219              165              170              175
221 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
222              180              185              190
224 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
225              195              200              205
227 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
228      210              215              220
230 Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu
231 225              230              235              240
233 Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
234      245              250              255
236 Val Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
237      260              265              270
239 Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
240      275              280              285
242 Leu His Asp Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
243      290              295              300
245 Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
246 305              310              315              320
248 Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
249      325              330              335
251 Tyr Val Glu Thr Arg Leu Ala Leu Ala Ala Asp Pro Thr Phe Cys Ala
252      340              345              350
254 Ser Leu Lys Ala Glu Leu Asp Leu Glu Glu Arg Val Met Gly Pro Arg
255      355              360              365
257 Cys Ser Gln Cys Asp Tyr Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
258      370              375              380
260 Met Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
261 385              390              395              400

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```

263 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
264          405          410          415
266 Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
267          420          425          430
269 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
270          435          440          445
272 Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
273          450          455          460
275 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
276 465          470          475          480
278 Phe Asn Gly Thr Leu Gln Leu Gln His Ser Lys Met Tyr Trp Pro Gly
279          485          490          495
281 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
282          500          505          510
284 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
285          515          520          525
287 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
288          530          535          540
290 Pro Cys Gly Lys Asp Gln Trp Ser Pro Glu Lys Ser Thr Thr Cys Leu
291 545          550          555          560
293 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
294          565          570          575
296 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
297          580          585          590
299 Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
300          595          600          605
302 Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
303          610          615          620
305 Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
306 625          630          635          640
308 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
309          645          650          655
311 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
312          660          665          670
314 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
315          675          680          685
317 Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
318          690          695          700
320 Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
321 705          710          715          720
323 Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
324          725          730          735
326 Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
327          740          745          750
329 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
330          755          760          765
332 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
333          770          775          780
335 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/725,037

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,3,4,6,7,8,11,12,13

Seq#:3; Xaa Pos. 1,3,4,7,9,10,11,13,14,15

Seq#:13; Xaa Pos. 120,121

Seq#:15; Xaa Pos. 8,15,59,62,76,117,128,136,168,173,175,176,203,226

VERIFICATION SUMMARY

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L:18 M:270 C: Current Application Number differs, Replaced Current Application Number
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:112
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15